



Figure 1A

Compd #	MOLSTRUCTURE
1	
2	
3	
4	
5	
6	
7	

Figure 1B

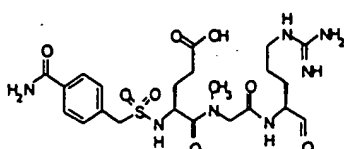
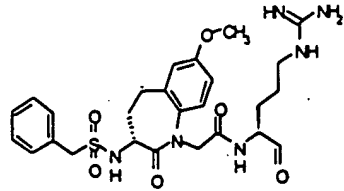
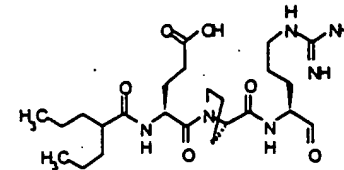
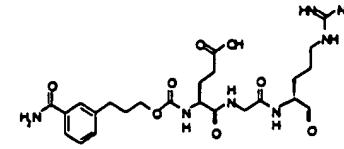
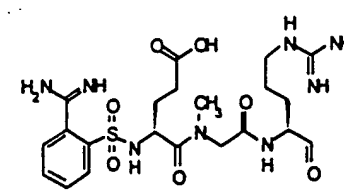
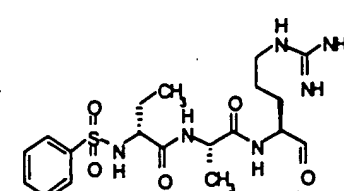
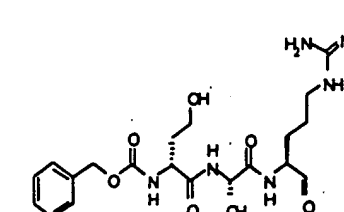
Compd #	MOLSTRUCTURE
8	
9	
10	
11	
12	
13	
14	

Figure 1C

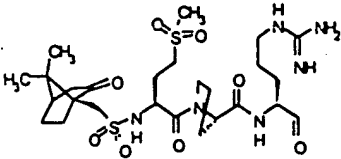
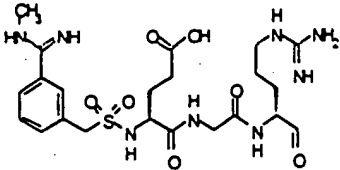
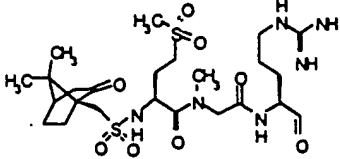
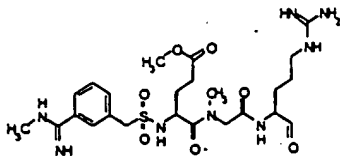
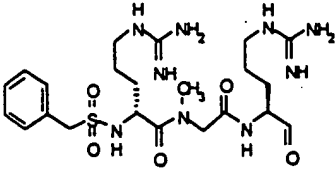
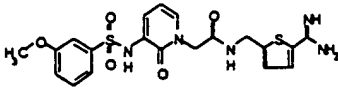
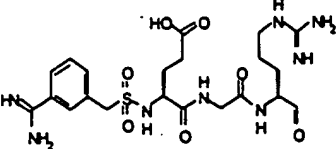
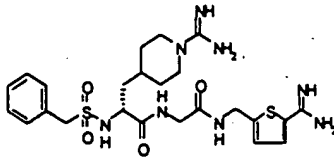
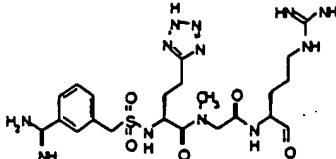
Compd #	MOLSTRUCTURE	Compd #	MOLSTRUCTURE
15		20	
16		21	
17		22	
18		23	
19			

FIGURE 2A

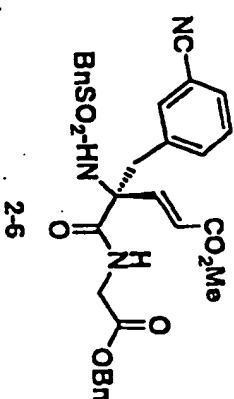
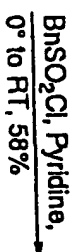
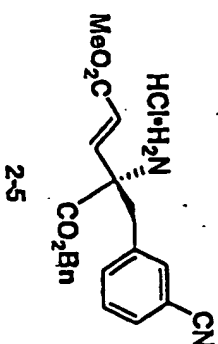
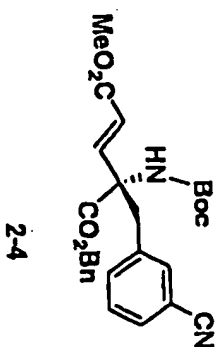
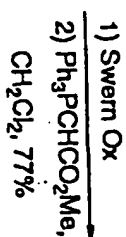
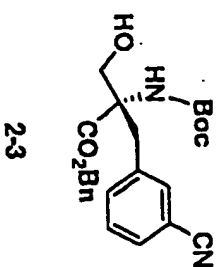
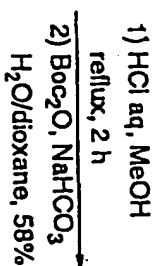
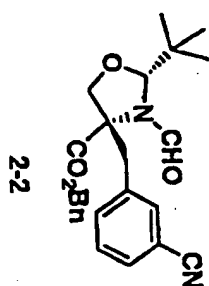
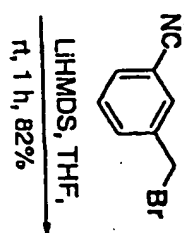
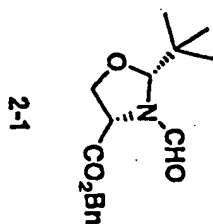
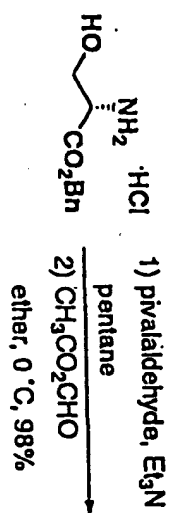


FIGURE 2B

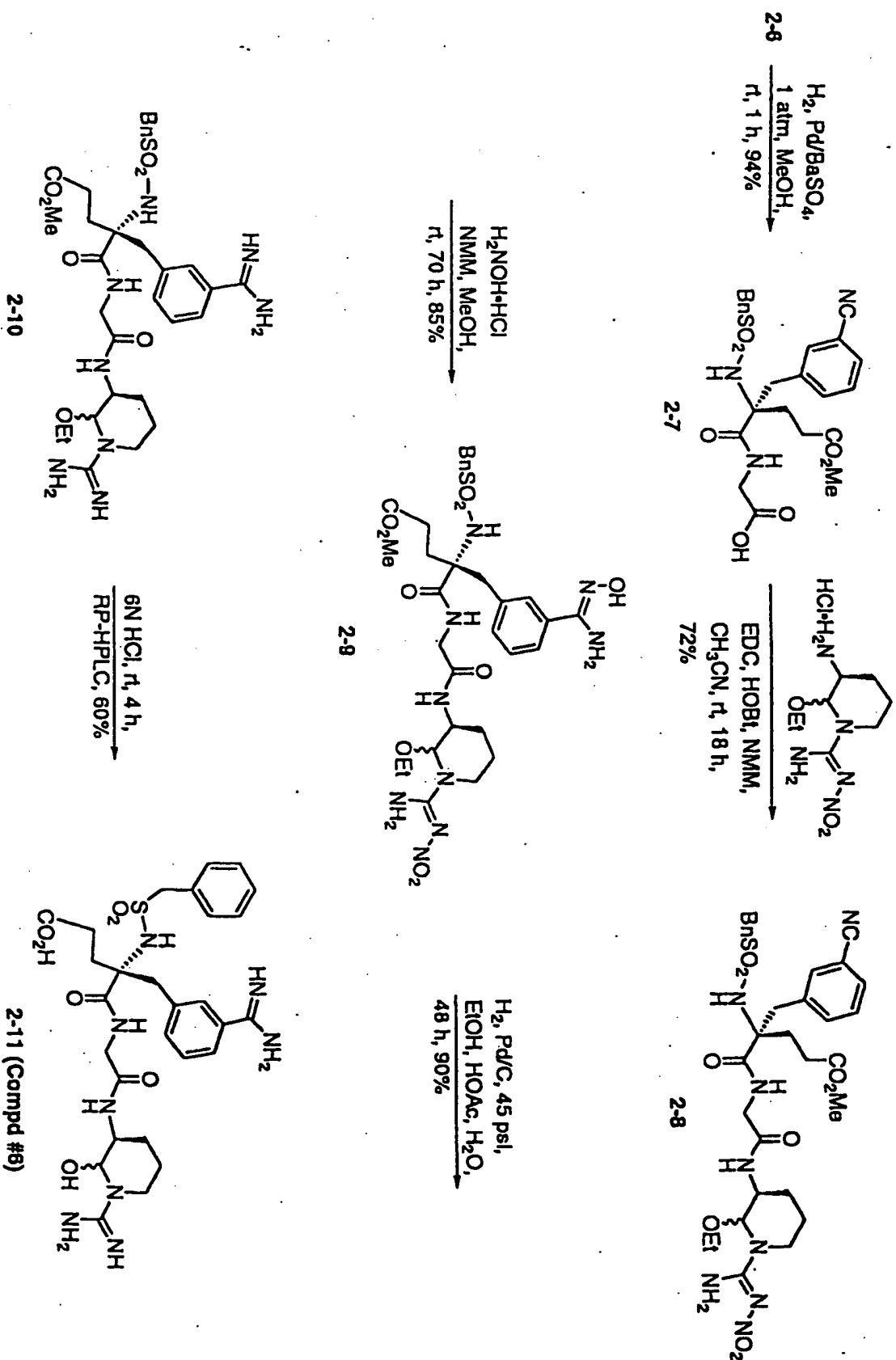


FIGURE 3A

10 20 30 40 50 60
GTTGTTGGGGGCACGGATGCGGATGAGGGCGAGTGGCCCTGGCAGGTAAGCCTGCATGCT
CAACAACCCCCGTGCCTACGCCTACTCCCGCTCACCGGGACCGTCCATTTCGGACGTACGA
V V G G T D A D E G E W P W Q V S L H A>
70 80 90 100 110 120
CTGGGCCAGGGCCACATCTGCGGTGCTTCCCTCATCTCTCCCAACTGGCTGGTCTCTGCC
GACCCGGTCCCGGTGTAGACGCCACGAAGGGAGTAGAGAGGGTTGACCGACCAGAGACGG
L G Q G H I C G A S L I S P N W L V S A>
130 140 150 160 170 180
GCACACTGCTACATCGATGACAGAGGATTGAGTACTCAGACCCACGCAGTGGACGGCC
CGTGTGACGATGTAGCTACTGTCTCCTAAGTCCATGAGTCTGGGGTGCGTCACCTGCCGG
A H C Y I D D R G F R Y S D P T Q W T A>
190 200 210 220 230 240
TTCCTGGGCTTGCACGACCAGAGCCAGCGCAGCGCCCCCTGGGGTGACAGAGCGCAGGCTC
AAGGACCCGAACGTGCTGGTCTCGGTGCGGTGCGGGGACCCACGTCCTCGCGTCCGAG
F L G L H D Q S Q R S A P G V Q E R R L>
250 260 270 280 290 300
AAGCGCATCATCTCCACCCCTTCTTCAATGACTTCACCTTCGACTATGACATCGCGCTG
TTCGCGTAGTAGAGGGTGGGGAAGAAGTTACTGAAGTGGAAGCTGATACTGTAGCGCGAC
K R I I S H P F F N D F T F D Y D I A L>
310 320 330 340 350 360
CTGGAGCTGGAGAAACCGGCAGAGTACAGCTCCATGGTGGCGCCCATCTGCCTGCCGGAC
GACCTCGACCTCTTTGGCCGTCTCATGTGAGGTACCACGCCGGGTAGACGGACGGCCTG
L E L E K P A E Y S S M V R P I C L P D>

FIGURE 3B

370 380 390 400 410 420
GCCTCCCATGTCTTCCCTGCCGGCAAGGCCATCTGGGTACGGGCTGGGGACACACCCAG
CGGAGGGTACAGAAGGGACGGCCGTTCCGGTAGACCCAGTGCCCGACCCCTGTGTGGGTC
A S H V F P A G K A I W V T G W G H T Q>

430 440 450 460 470 480
TATGGAGGCACTGGCGCGCTGATCCTGCAAAAGGGTGAGATCCGCGTCATCAACCAGACC
ATACCTCCGTGACCGCGCGACTAGGACGTTTCCCACTCTAGGCGCAGTAGTTGGTCTGG
Y G G T G A L I L Q K G E I R V I N Q T>

490 500 510 520 530 540
ACCTGCGAGAACCTCCTGCCGCAGCAGATCACGCCGCGCATGATGTGCGTGGGCTTCCTC
TGGACGCTCTTGGAGGACGGCGTCTAGTGCGGCGCGTACTACACGCACCCGAAGGAG
T C E N L L P Q Q I T P R M M C V G F L>

550 560 570 580 590 600
AGCGGCGGCGTGGACTCCTGCCAGGGTGATTCCGGGGGACCCCTGTCCAGCGTGGAGGCG
TCGCCGCCGCACCTGAGGACGGTCCCACTAAGGCCCCCTGGGGACAGGTCGCACCTCCGC
S G G V D S C Q G D S G G P L S S V E A>

610 620 630 640 650 660
GATGGGCGGATCTTCCAGGCCGGTGTGGTGAGCTGGGGAGACGGCTGCGCTCAGAGGAAC
CTACCCGCCTAGAAGGTCCGGCCACACCACTCGACCCCTCTGCCGACGCGAGTCTCCTTG
D G R I F Q A G V V S W G D G C A Q R N>

670 680 690 700 710 720
AAGCCAGGCGGTACACAAGGCTCCCTCTGTTTCGGGACTGGATCAAAGAGAACACTGGG
TTCGGTCCGCACATGTGTTCCGAGGGAGACAAAGCCCTGACCTAGTTTCTTGTGACCC
K P G V Y T R L P L F R D W I K E N T G>

FIGURE 3C

GTATAG

CATATC

V *>